

WO 00/34448

SEQUENCE LISTING

<110> E. I. DU PONT DE NEMOURS AND COMPANY
<120> PLANT 1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE
<130> BB1297

<140>
<141>

<150> 60/110,865
<151> 1998-DECEMBER-04

<160> 22

<170> Microsoft Office 97

<210> 1
<211> 565
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (5)..(9)

<220>
<221> unsure
<222> (450)

<220>
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<222> (549)

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ccctccctct ccccctccctc gcccagcgcc aattaccaca gcctcccccag caagccggga 180
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gcaggggacc ttcgtccag cacaaagtgg attttacgtt tcaaaggaag ggcaaacgag 300
ctatttcaactt gagaaggaca tgctgttcta tgcaacaggc tccaccacca gcatggcctg 360
ggcgagctgt tgctgagcctt ggccggagtc atgggatggc ccaaagccta tctcgattgt 420
tggttcaactt ggttccatagt gaacacagan attggacattt gttgcggaga atcctgataa 480
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<210> 2
<211> 63
<212> PRT
<213> Zea mays

<220>
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<222> (25)

<220>
<221> UNSURE
<222> (58)

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Ser Thr Gly Ser Ile Gly Thr Gln Xaa Leu Asp Ile Val Ala Glu Asn
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Pro Asp Lys Phe Arg Val Val Ala Leu Ala Ala Gly Ser Asn Val Thr
 35 40 45

Leu Leu Ala Asp Gln Val Lys Thr Phe Xaa Pro Lys Leu Val Arg
 50 55 60

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 <212> DNA
 <213> Zea mays

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 ggttgtcag ggctgaagcc tacagttgtc gcaattgaag ctgttaaaga catagcattt 180
 gcaaaacaaag agacacttat tgcaggttgtt ctttttgtc ttccccttgc acacaaacac 240
 aaagtgaaaa ttcttccagc tgattctgag cactctgaa tatttcagtg tatacaaggc 300
 ttgtccgaag gtgcacttcg tcgcattt ctaactgcat cangtggc tttcanggac 360
 tggccantt acaggctgaa agatgtaaaa gttgctgacg ctttaaagca tccaaactgg 420
 aatatggaa ggaagatcac agtagattct gctactttt tcaacaaggg tttagaagtt 480
 attgaagcac attattttt tggctgtgaa tatgtatgaca ttgagattgt gattcaccca 540
 cagtctatca tacactctat ggtgaaacc caggattcat ctgtccttagc tcagttggg 600
 tggccagata tgcggattacc aatcttatac accttatacat ggccagatag gagtcctgag 660
 cgctgctaat gagaaggccg tggagttgtt cattgacgag aagatttagct acctggacat 720
 attcaaggtg gtggagctt catgtAACGC gcatcggAAC agctggtaac aaccgtcact 780
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<210> 4
 <211> 217
 <212> PRT
 <213> Zea mays

<220>

<221> UNSURE
<222> (115)

<220>

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<220>

<221> UNSURE
<222> (123)

<400> 4

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20 25 30Val Thr Val Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr
35 40 45Val Ala Ala Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu
50 55 60Thr Leu Ile Ala Gly Gly Pro Phe Val Leu Pro Leu Ala His Lys His
65 70 75 80Lys Val Lys Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln
85 90 95Cys Ile Gln Gly Leu Ser Glu Gly Ala Leu Arg Arg Ile Ile Leu Thr
100 105 110Ala Ser Xaa Gly Ala Phe Xaa Asp Trp Pro Xaa Asp Arg Leu Lys Asp
115 120 125Val Lys Val Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Arg
130 135 140Lys Ile Thr Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val
145 150 155 160Ile Glu Ala His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile
165 170 175Val Ile His Pro Gln Ser Ile Ile His Ser Met Val Glu Thr Gln Asp
180 185 190Ser Ser Val Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile
195 200 205Leu Tyr Thr Leu Ser Trp Pro Asp Arg
210 215

<210> 5

<211> 1901

<212> DNA

<213> Oryza sativa

<210> 6
<211> 473
<212> PRT
<213> Orgy

<400> 6

Met Ala Leu

1

The Law As

Low-Beta Rh

Sue, Sue, Sue

50

Val Val C14

69

The Val. Class

Ala-Glu-Aga

Asn Val Thr Leu Leu Ala Asp Gln Val Lys Thr Phe Lys Pro Lys Leu
 115 120 125
 Val Ala Val Arg Asn Glu Ser Leu Val Asp Glu Leu Lys Glu Ala Leu
 130 135 140
 Ala Asp Cys Asp Trp Lys Pro Glu Ile Ile Pro Gly Glu Gln Gly Val
 145 150 155 160
 Ile Glu Val Ala Arg His Pro Asp Ala Val Thr Val Val Thr Gly Ile
 165 170 175
 Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu Ala Gly
 180 185 190
 Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly Gly Pro
 195 200 205
 Phe Val Leu Pro Leu Ala Gln Lys His Lys Val Lys Ile Leu Pro Ala
 210 215 220
 Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu Pro Glu
 225 230 235 240
 Gly Ala Leu Arg Arg Ile Ile Leu Thr Ala Ser Gly Gly Ala Phe Arg
 245 250 255
 Asp Trp Pro Val Asp Lys Leu Lys Glu Val Lys Val Ala Asp Ala Leu
 260 265 270
 Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr Val Asp Ser Ala
 275 280 285
 Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr Leu Phe
 290 295 300
 Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His Pro Gln Ser Ile
 305 310 315 320
 Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val Leu Ala Gln Leu
 325 330 335
 Gly Trp Pro Asp Met Arg Ile Pro Thr Leu Tyr Thr Met Ser Trp Pro
 340 345 350
 Asp Arg Ile Tyr Cys Ser Glu Val Thr Trp Pro Arg Leu Asp Leu Cys
 355 360 365
 Lys Leu Gly Ser Leu Thr Phe Lys Ala Pro Asp Asn Val Lys Tyr Pro
 370 375 380
 Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly Gly Thr Met Thr
 385 390 395 400
 Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu Leu Phe Ile Asp
 405 410 415
 Glu Lys Ile Gly Tyr Leu Asp Ile Phe Lys Val Val Glu Leu Thr Cys
 420 425 430

Asp Ala His Arg Asn Glu Leu Val Thr Arg Pro Ser Leu Glu Glu Ile
 435 440 445

Ile His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala Ser Leu Gln Pro
 450 455 460

Ser Thr Gly Leu Ser Pro Val Pro Val
 465 470

<210> 7

<211> 1592

<212> DNA

<213> Glycine max

<220>

<221> unsure

<222> (993)

<220>

<221> unsure

<222> (1402)

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agtgcacacaa cagtagagag acgagtttat tgctctgccc ctgctcaatc	accaccacca	180
gcattggccag gaacagctat tcccgagctt tctgatttca agacatggga	tgggcaaaaa	240
cctatttctg tcttaggatc tacgggttca attggaactc agacactgag	tatagtggct	300
gagttcccag aaagattttaa agttgtgagc cttgctgctg gctctaataat	tactcttctt	360
gctgaccaga ttaaaacatt taagcctgaa gttgttggtc ttagaaatgaa	gtctttaatt	420
gatgaactca aagaggctt ggctgatgtg gatcacaac ccgaaatcat	ccctggagag	480
caaggagtca ttgaggccgc tcgtcaccct gatgccacca ctgttagttac	aggcatagtt	540
ggttgtcag gattaaagcc aacagttgca gcaatttgaag caggaaaaga	catagcattt	600
gccaacaaaag agacaatgat tgccggagcc ctttttggtc ttcccttgc	tcacaaacat	660
aacataaaaa ttcttccgc tgattcggaa cattctgcaa ttttcagtc	tatccagggg	720
ttgccaaagg gtgcacttag gaaaatcctt ttaactggat caggagggtc	tttcagagaa	780
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agtttggga gaaaaataac tattgactct gctaccctt tcaataaggg	tctagaagta	900
attgaagcac attacttgc tggagcaagc tatgacgata ttgagattgt	tattcatcct	960
caatccatca tacattcctt ggttggaaacg cangattcat ctgttaatgc	acagttgggg	1020
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tctgaagtaa cttggcctcg tcttgcattt agcaagtatg gttctctaac	attttatgca	1140
ccggatgaca agaagttcc atcggtaat ctttgctatg ctgcgggacg	tgctggaggc	1200
accatgacag gagttcttag tgcagcaaat gagaaagctg tagaaatgtt	tgttgaagaa	1260
aagatttagtt atctggatattt atccaagggtt gtggaactaa cttgtcagga	acatccaaaag	1320
gaatttagtag catctccgtc actcgaagaa attatttcaat atgaccaatg	ggctcgacaa	1380
tatgctgcta gtctgcaaaa angttcaag tgtttgaatc ccatatttct	gacatatttt	1440
agaagttggg gctgtgggg attgttggca actgctagca tattttgtaa	atgtattgtt	1500
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<210> 8

<211> 499

<212> PRT

<213> Glycine max

<220>

<221> UNSURE

<222> (325)

<220>

<221> UNSURE
<222> (462)

<400> 8

Met Ala Leu Asn Leu Pro Ser Pro Ala Gln Val Lys Pro Leu Phe Phe
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Ser Ser Asn Asn Ser Thr Lys Leu Pro Gly Ser Phe Ser Leu Lys Arg
20 25 30

Lys Asp Ser Asp Thr Thr Val Glu Arg Arg Val Tyr Cys Ser Ala Ala
35 40 45

Ala Gln Ser Pro Pro Pro Ala Trp Pro Gly Thr Ala Ile Pro Glu Pro
50 55 60

Ser Asp Phe Lys Thr Trp Asp Gly Gln Lys Pro Ile Ser Val Leu Gly
65 70 75 80

Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Ser Ile Val Ala Glu Phe
85 90 95

Pro Glu Arg Phe Lys Val Val Ser Leu Ala Ala Gly Ser Asn Ile Thr
100 105 110

Leu Leu Ala Asp Gln Ile Lys Thr Phe Lys Pro Glu Val Val Gly Leu
115 120 125

Arg Asn Glu Ser Leu Ile Asp Glu Leu Lys Glu Ala Leu Ala Asp Val
130 135 140

Asp His Lys Pro Glu Ile Ile Pro Gly Glu Gln Gly Val Ile Glu Ala
145 150 155 160

Ala Arg His Pro Asp Ala Thr Thr Val Val Thr Gly Ile Val Gly Cys
165 170 175

Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu Ala Gly Lys Asp Ile
180 185 190

Ala Leu Ala Asn Lys Glu Thr Met Ile Ala Gly Ala Pro Phe Val Leu
195 200 205

Pro Leu Ala His Lys His Asn Ile Lys Ile Leu Pro Ala Asp Ser Glu
210 215 220

His Ser Ala Ile Phe Gln Ser Ile Gln Gly Leu Pro Lys Gly Ala Leu
225 230 235 240

Arg Lys Ile Leu Leu Thr Gly Ser Gly Gly Ala Phe Arg Glu Trp Pro
245 250 255

Ala Glu Lys Met Lys Asp Ile Lys Leu Ala Asp Ala Leu Lys His Pro
260 265 270

Ile Trp Ser Leu Gly Arg Lys Ile Thr Ile Asp Ser Ala Thr Leu Phe
275 280 285

Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr Leu Phe Gly Ala Ser
 290 295 300
 Tyr Asp Asp Ile Glu Ile Val Ile His Pro Gln Ser Ile Ile His Ser
 305 310 315 320
 Leu Val Glu Thr Xaa Asp Ser Ser Val Asn Ala Gln Leu Gly Ile Pro
 325 330 335
 Asp Met Arg Leu Pro Leu Leu Tyr Thr Leu Ser Trp Pro Glu Arg Ile
 340 345 350
 Tyr Cys Ser Glu Val Thr Trp Pro Arg Leu Asp Leu Ser Lys Tyr Gly
 355 360 365
 Ser Leu Thr Phe Tyr Ala Pro Asp Asp Lys Lys Phe Pro Ser Val Asn
 370 375 380
 Leu Cys Tyr Ala Ala Gly Arg Ala Gly Gly Thr Met Thr Gly Val Leu
 385 390 395 400
 Ser Ala Ala Asn Glu Lys Ala Val Glu Met Phe Val Glu Glu Lys Ile
 405 410 415
 Ser Tyr Leu Asp Ile Phe Lys Val Val Glu Leu Thr Cys Gln Glu His
 420 425 430
 Gln Lys Glu Leu Val Ala Ser Pro Ser Leu Glu Glu Ile Ile His Tyr
 435 440 445
 Asp Gln Trp Ala Arg Gln Tyr Ala Ala Ser Leu Gln Lys Xaa Phe Lys
 450 455 460
 Cys Leu Asn Pro Ile Phe Leu Thr Tyr Phe Arg Ser Trp Gly Cys Gly
 465 470 475 480
 Gly Leu Leu Ala Thr Ala Ser Ile Phe Cys Lys Cys Ile Val Gly Ser
 485 490 495
 Ser Ile Leu

<210> 9
 <211> 784
 <212> DNA
 <213> Glycine max

 <220>
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 <222> (772)

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 <222> (779)..(780)

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 actgggtCAA ttggAACTCA gacactagat attgtgcag agaATCCAGA taagttaaa 180
 gttgtggcac ttgcagctgg ttcaaATGTT actcttcttG cagaccAGGT aaaaAGATT 240
 aagcctcaac ttgttgcgt tagaaatgag tccctaattG ctgaacttGA agaggcTTG 300
 catgtatTTG aagaaaaacc tgagatcatc cctggagAGC aggaaATCAT tgaggttgct 360
 cgtcacccAG atgcagttag tgttagtcaca ggaatAGTAG gctgtgcagg actgaAGCCA 420
 acagtgcag cgatagaAGC agggAAAGAC atagcttgg ccaacAAAGA gacattGATT 480
 gctggaggTC ctttgttCTC ctcttgctca gaagcataat gtaaaaATAC ttccagctGA 540
 ttcagaACAT ctgCCatCTT tcagtgtatC caggggttGC cagagggtGC acttaggAGA 600
 gttatTTAA ctgcATctgg aggtgcTTtC aggggatGGC cagttggata actgaAGANG 660
 ttAAAGTtGC tgatnCatta aaacatCCTA ctggaaatATG ggggAAAGAA ctgtggACTC 720
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 catt 784

<210> 10
 <211> 215
 <212> PRT
 <213> Glycine max

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 <222> (19)

<220>
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 <222> (183)

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 Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr
 35 40 45
 Leu Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Lys Val Val Ala Leu
 50 55 60
 Ala Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Lys Arg Phe
 65 70 75 80
 Lys Pro Gln Leu Val Ala Val Arg Asn Glu Ser Leu Ile Ala Glu Leu
 85 90 95
 Glu Glu Ala Leu His Asp Val Glu Glu Lys Pro Glu Ile Ile Pro Gly
 100 105 110
 Glu Gln Gly Ile Ile Glu Val Ala Arg His Pro Asp Ala Val Ser Val
 115 120 125
 Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala
 130 135 140
 Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile
 145 150 155 160
 Ala Gly Gly Pro Leu Ser Pro Leu Ala Gln Lys His Asn Val Lys Ile
 165 170 175
 Leu Pro Ala Asp Ser Asp Xaa Ser Ala Ile Phe Gln Cys Ile Gln Gly
 180 185 190
 Leu Pro Glu Gly Ala Leu Arg Arg Val Ile Leu Thr Ala Ser Gly Gly
 195 200 205
 Ala Phe Arg Gly Trp Pro Val
 210 215
 <210> 11
 <211> 642
 <212> DNA
 <213> *Triticum aestivum*
 <220>
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<220>
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<222> (628)

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tgcctacctg aggacatgtc gtcctatgca gcagggccca ccgccccgcct ggccaggccg 180
agccgtcggtg gaacctgaga ggaggtcggtg ggagggccca aagccccatct ccatcgtcgg 240
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ccgggttgcc gccccttgctg ctgggtccaa cgtcactcct ctatgtata aggtgaaaac 360
gttcaaaacca aactgggtgg tgttaagaaa cgatccatta ctaacgagc taaaggaagc 420
attaactgggt tgtgaaagag atccggatta tccctggga caagtgcata gaggcgcacc 480
cacccggacc attacatcct tacgggnatata aggttncaag atcaacctac attncaacat 540
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naacanatttga aataactctg cgatnaanat ctgatatcat ga 642

<210> 12
<211> 94
<212> PRT
<213> *Triticum aestivum*

<400> 12
 Met Gln Gln Gly Pro Pro Pro Ala Trp Pro Gly Arg Ala Val Val Glu
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 Pro Glu Arg Arg Ser Trp Glu Gly Pro Lys Pro Ile Ser Ile Val Gly
 20 25 30
 Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Asp Ile Val Ala Glu Asn
 35 40 45
 Leu Thr Ser Ser Arg Val Val Ala Leu Ala Ala Gly Ser Asn Val Thr
 50 55 60
 Pro Leu Ala Asp Lys Val Lys Thr Phe Lys Pro Asn Trp Val Val Leu
 65 70 75 80
 Arg Asn Asp Pro Leu Leu Asn Glu Leu Lys Glu Ala Leu Thr
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 <210> 13
 <211> 360
 <212> DNA
 <213> *Triticum aestivum*

 <220>
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 <222> (295)

 <220>
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 <220>
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 <220>
 <221> unsure
 <222> (338)

 <220>
 <221> unsure
 <222> (352)

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 gtacgcggca gggcgagccg ggggcaccat gacgggattt ttgagtgctg ctaatgagaa 240
 ggcgtggagc ttgttcatcg acgaaaagat taactacctt ggacatcttc aaggngggng 300
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 <212> PRT
 <213> *Triticum aestivum*

 <220>
 <221> UNSURE
 <222> (59)

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Tyr Thr Leu Ser Trp Pro Asp Arg Val Tyr Cys Ser Glu Val Thr Trp
 20 25 30

Pro Arg Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Ala Pro
 35 40 45

Asp Asn Val Lys Tyr Pro Ser Val Asp Leu Xaa Xaa Tyr Ala Ala Gly
 50 55 60

Arg Ala Gly Gly Thr Met Thr Gly Phe Leu Ser Ala Ala Asn Glu Lys
 65 70 75 80

Ala Trp Ser Leu Phe Ile Asp Glu Lys Ile Asn Tyr Leu
 85 90

<210> 15

<211> 1847

<212> DNA

<213> Zea mays

<220>

<221> unsure

<222> (5)..(9)

<400> 15

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 aaggccttggc tgattgcgaa gagaaggccatc aaattattcc tggggagcaaa ggtgtcatag 660
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 gcccgtcactt ggaggagatc gtccattacat atctgtgggc gaggagatat gcaagccatc 1560
 tacaaccatc ttctggccctt agccctgtcc ctgcataata ggtcgtcagc acaacgttgt 1620
 acagcaggag ttctaaagata tgatgtgtttt gtggctcctt tttccatgtt caatttcag 1680
 gcctccacat gaataaaaatcg catctattcc atgtgatttc ttttatggat gaagtgtgcg 1740

aagtccgggtg ggaatcagat gcatccctt cggtgagtt cttacgtagg gttgagcagc 1800
 attttttaaa aaggttttt tacctctgca aaaaaaaaaa aaaaaaaaaa 1847

<210> 16
 <211> 472
 <212> PRT
 <213> Zea mays

<400> 16
 Met Ala Ala Leu Lys Ala Ser Phe Arg Gly Glu Leu Ser Ala Ala Ser
 1 5 10 15

Phe Leu Asp Ser Ser Arg Gly Pro Leu Val Gln His Lys Val Asp Phe
 20 25 30

Thr Phe Gln Arg Lys Gly Lys Arg Ala Ile Ser Leu Arg Arg Thr Cys
 35 40 45

Cys Ser Met Gln Gln Ala Pro Pro Pro Ala Trp Pro Gly Arg Ala Val
 50 55 60

Ala Glu Pro Gly Arg Arg Ser Trp Asp Gly Pro Lys Pro Ile Ser Ile
 65 70 75 80

Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Asp Ile Val Ala
 85 90 95

Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu Ala Ala Gly Ser Asn
 100 105 110

Val Thr Leu Leu Ala Asp Gln Val Lys Thr Phe Lys Pro Lys Leu Val
 115 120 125

Ala Val Arg Asn Glu Ser Leu Val Asp Glu Leu Lys Glu Ala Leu Ala
 130 135 140

Asp Cys Glu Glu Lys Pro Glu Ile Ile Pro Gly Glu Gln Gly Val Ile
 145 150 155 160

Glu Val Ala Arg His Pro Asp Ala Val Thr Val Val Thr Gly Ile Val
 165 170 175

Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu Ala Gly Lys
 180 185 190

Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly Gly Pro Phe
 195 200 205

Val Leu Pro Leu Ala His Lys His Lys Val Lys Ile Leu Pro Ala Asp
 210 215 220

Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu Ser Glu Gly
 225 230 235 240

Ala Leu Arg Arg Ile Ile Leu Thr Ala Ser Gly Gly Ala Phe Arg Asp
 245 250 255

Trp Pro Val Asp Arg Leu Lys Asp Val Lys Val Ala Asp Ala Leu Lys
 260 265 270

His Pro Asn Trp Asn Met Gly Arg Lys Ile Thr Val Asp Ser Ala Thr
 275 280 285
 Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr Leu Phe Gly
 290 295 300
 Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His Pro Gln Ser Ile Ile
 305 310 315 320
 His Ser Met Val Glu Thr Gln Asp Ser Ser Val Leu Ala Gln Leu Gly
 325 330 335
 Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr Leu Ser Trp Pro Asp
 340 345 350
 Arg Ile Tyr Cys Ser Glu Val Thr Trp Pro Arg Leu Asp Leu Cys Lys
 355 360 365
 Leu Gly Ser Leu Thr Phe Arg Ala Pro Asp Asn Val Lys Tyr Pro Ser
 370 375 380
 Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly Gly Thr Met Thr Gly
 385 390 395 400
 Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu Leu Phe Ile Asp Glu
 405 410 415
 Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val Glu Leu Thr Cys Asn
 420 425 430
 Ala His Arg Asn Glu Leu Val Thr Ser Pro Ser Leu Glu Ile Val
 435 440 445
 His Tyr Asp Leu Trp Ala Arg Arg Tyr Ala Ala Ser Leu Gln Pro Ser
 450 455 460
 Ser Gly Leu Ser Pro Val Pro Ala
 465 470

<210> 17
 <211> 2019
 <212> DNA
 <213> Glycine max

<400> 17
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 tttcgtgtat tccttcaagt ctaactgcct cacagcaaaa ttctcagggtg ggtttgtttt 180
 taagagaaaa gagcgttagag cagcatctgg aggacgggtt tattgctcaag tgcaggcaac 240
 accaccacca ccagcctggc cgggacgagc ggttccggaa caaggtcgca agacttggga 300
 tggaccaaaa cccatttcaa ttgtggggag tactggttca atttggaaactc agacactaga 360
 tattgtggca gagaatccag ataagttaa agttgtggca ctgcagctg gttcaaatgt 420
 tactcttctt gcagaccagg taaaaagatt taagcctcaa ctgttgcgtt ttagaaatga 480
 gtcccttaatt gctgaacttg aagaggccctt gcatgatgtt gaagaaaaac ctgagatcat 540
 ccctggagag cagggaatca ttgaggttgc tcgtcacccca gatgcagttt gtgtagtcac 600
 aggaatagta ggctgtgcag gactgaagcc aacagttgca gcgatagaag cagggaaaga 660
 catagcttgc gccaacaaag agacattgtat tgctggaggt cctttgttc ttccttgc 720
 tcagaagcat aatgtaaaaa tacttccagc tgattcagaa cattctgcca tctttcagtg 780
 tatccagggg ttgcccagagg gtgcacttag gagagttatt ttaactgcat ctggaggtgc 840
 ttccaggat tggccagttg ataaactgaa agatgttaaa gttgctgatg cattaaaaca 900

tccttaactgg aatatgggaa aaaagataac tggactct gctacccttt ttaataaggg 960
 tctagaagta attgaagcac attacttgg tggagctgac tacgatcata ttgagattgt 1020
 cattcatcca caatcaatca tacattcaat gattgaaaca caggattcat ctgttcttgc 1080
 acaattgggg tggcctgata tgcgttgcc aatcctctat acattatcat ggcctgacag 1140
 gatttattgt tctgaagtca cttggccacg ctttgatctt tgcagcttg gttcaacttac 1200
 atttaaaaact ccagataatg taaaatgttcc atccatgaat ctgcattttt ctgctggccg 1260
 tgctggaggc acaatgacag gagttcttag tgcagcaaat gaaaaagctg tagagatgtt 1320
 tattgatgaa aagataagttt attgaaatatttcaatgtt gttggagctaa catgtgagaa 1380
 gcatcaaaaat gaattggat ccttccttc ctttgaggaa attatttcaactt atgacactgt 1440
 ggcgcgaaaa tatgctgcta gtctgcaaga ctcttccagc ttcaacttca ttcttgcatt 1500
 agatgatta aactaggat gtggctgatg ctcccattt gcctgcttcc accataattt 1560
 ctgcggcat tgaacaatgtt agaatggtc attccacaga tggtaaaaat taaataggtt 1620
 ttttggttat gaaatgttgg tggtaaca ctttcaattt gatcttataat ttttgcgtt 1680
 atttcatgga aacatgttcc tttttaatag tcaataggag cctaggaggt tggttgggtt 1740
 cctatgaatgt tgcataatgtt aagaaggaa atggattttt tcatatttcaaa aatttacatg 1800
 atgtggtcaa ctagaagttt tgcatttttcaat agaattaaat aggtggagtc 1860
 ttacaaaaat taacagagat agacacaaaa gttgaccaat caccaatcac tttcataaaaa 1920
 ggattccctt tcttttctt cagcacacat tgcgttggctt atattattat atgaaattgg 1980
 tattatttgg atatcatagc taaaaaaaaaaa aaaaaaaaaa 2019

<210> 18

<211> 475

<212> PRT

<213> Glycine max

<400> 18

Met Met Ala Leu Asn Ile Ser Ser Pro Ala Glu Val Lys Ser Ile Phe
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Phe Ala Asp Ser Phe Lys Ser Asn Cys Leu Thr Ala Lys Phe Ser Gly
 20 25 30

Gly Phe Ala Phe Lys Arg Lys Glu Arg Arg Ala Ala Ser Gly Gly Arg
 35 40 45

Val Tyr Cys Ser Val Gln Ala Thr Pro Pro Pro Pro Ala Trp Pro Gly
 50 55 60

Arg Ala Val Pro Glu Gln Gly Arg Lys Thr Trp Asp Gly Pro Lys Pro
 65 70 75 80

Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Asp
 85 90 95

Ile Val Ala Glu Asn Pro Asp Lys Phe Lys Val Val Ala Leu Ala Ala
 100 105 110

Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Lys Arg Phe Lys Pro
 115 120 125

Gln Leu Val Ala Val Arg Asn Glu Ser Leu Ile Ala Glu Leu Glu Glu
 130 135 140

Ala Leu His Asp Val Glu Glu Lys Pro Glu Ile Ile Pro Gly Glu Gln
 145 150 155 160

Gly Ile Ile Glu Val Ala Arg His Pro Asp Ala Val Ser Val Val Thr
 165 170 175

Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu
 180 185 190
 Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly
 195 200 205
 Gly Pro Phe Val Leu Pro Leu Ala Gln Lys His Asn Val Lys Ile Leu
 210 215 220
 Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu
 225 230 235 240
 Pro Glu Gly Ala Leu Arg Arg Val Ile Leu Thr Ala Ser Gly Gly Ala
 245 250 255
 Phe Arg Asp Trp Pro Val Asp Lys Leu Lys Asp Val Lys Val Ala Asp
 260 265 270
 Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr Val Asp
 275 280 285
 Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr
 290 295 300
 Leu Phe Gly Ala Asp Tyr Asp His Ile Glu Ile Val Ile His Pro Gln
 305 310 315 320
 Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val Leu Ala
 325 330 335
 Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr Leu Ser
 340 345 350
 Trp Pro Asp Arg Ile Tyr Cys Ser Glu Val Thr Trp Pro Arg Leu Asp
 355 360 365
 Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Thr Pro Asp Asn Val Lys
 370 375 380
 Tyr Pro Ser Met Asn Leu Ala Phe Ser Ala Gly Arg Ala Gly Gly Thr
 385 390 395 400
 Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu Met Phe
 405 410 415
 Ile Asp Glu Lys Ile Ser Tyr Trp Asn Leu Phe Lys Val Val Glu Leu
 420 425 430
 Thr Cys Glu Lys His Gln Asn Glu Leu Val Ser Ser Pro Ser Leu Glu
 435 440 445
 Glu Ile Ile His Tyr Asp Leu Trp Ala Arg Lys Tyr Ala Ala Ser Leu
 450 455 460
 Gln Asp Ser Ser Ser Phe Thr Pro Ile Leu Ala
 465 470 475
 <210> 19
 <211> 1640

<212> DNA

<213> *Triticum aestivum*

<400> 19

gcacgagctc cttctccctc ctcgagctct cctccggcac caccaggagc aggaggggag 60
 ccgccttccg ccccegcag caccagegca aagtggactt gacgttcaa aggagggaca 120
 aaagagcagc ctacctgagg acatgctgct ccatgcagca gggcccaccc cccgcctggc 180
 ctggccgagc cgtcgcgaa cccgagagga ggtcggtggg gggccccaaag cccatctcga 240
 tcgtcggctc aaccggttcc ataggaacac agacattgga catcggtcg gagaatcctg 300
 acaaggctcg ggttgcgtct ctgcgtctg gtcctaattgt cactcttcta gctgatcagg 360
 tgaaaacgtt caagccaaag ctgtgtggctg taagaaacga gtcattactt aacgagctaa 420
 aggaagcgtt agctgggtgt gaagaaatgc cggaaattat tcctggggag caagggtgtca 480
 tagaggtcgc tcgcccacccg gatgcagtta cagtcgttac gggcatagta ggggtgtcag 540
 gactcaagcc tacagttgca gcaattgaag ctgggaaaga tattgcgtt gcgaacaaag 600
 agacacttat cgcaggcggt ccgttcgtgc ttccccttgc gcacaagcac aatgtgaaaa 660
 tacttcctgc tgattcagag cactctgcaa tatttcagtg tatacagggc ttgtctgaag 720
 gatcaacttcg tcgcgttatt ctgactgcgt ctggcgttgc ttcaaggagc tggccagttg 780
 agaaggtgaa agatgtaaaag gttgccatg ctttgaagca cccaaactgg agcatggga 840
 agaaaatcac agtagattct gctactttgt tcaacaaggg gtttagaagtt atcgaggcgc 900
 attatttgtt tgggtgtgaa tatgatgaca ttgagattgt gattcaccca cagtcacatca 960
 tacactctat gattgaaaacc caggattcat ctgtccttgc tcagctggg tggccagaca 1020
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 cctggccccc gctagacctt tgcaagctgg gttcgctgac attaaagct cccgacaaacg 1140
 tgaataaccc atcgggtgat ctcgcgtat cggcaggcg gcccggggc accatgacgg 1200
 gagttttag tgcgtctaatt gagaaggcgg tggagctgtt catcgacgaa aagatcagct 1260
 acctggacat cttcaaggtg gtggagatga cgtgcgacgc gcacccgcaac gagctggta 1320
 caaggccgtc gtcgaggag atcatacatt acgaccagtg gccaaggaag tttgccgcca 1380
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 gctggccgat gaagcacaga agatgtagcc atggccttgc ctgtctaaaa ctggccatgt 1500
 gggaaaccaag ctttagatatt tcaacaaggc acacataagg tgccttccag aaatgtaaat 1560
 catgtgttgg cacgaataaaa tcatgttaagt ttgtatggat ggatgaaata ggcaaggaat 1620
 caaa 1640

<210> 20

<211> 473

<212> PRT

<213> *Triticum aestivum*

<400> 20

Thr	Ser	Ser	Phe	Ser	Leu	Leu	Glu	Leu	Ser	Ser	Gly	Thr	Thr	Arg	Ser
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Arg	Arg	Gly	Ala	Ala	Phe	Arg	Pro	Arg	Gln	His	Gln	Arg	Lys	Val	Asp
					20				25				30		

Leu	Thr	Phe	Gln	Arg	Arg	Asp	Lys	Arg	Ala	Ala	Tyr	Leu	Arg	Thr	Cys
						35		40				45			

Cys	Ser	Met	Gln	Gln	Gly	Pro	Pro	Pro	Ala	Trp	Pro	Gly	Arg	Ala	Val
						50		55			60				

Ala	Glu	Pro	Glu	Arg	Arg	Ser	Trp	Glu	Gly	Pro	Lys	Pro	Ile	Ser	Ile
						65		70		75		80			

Val	Gly	Ser	Thr	Gly	Ser	Ile	Gly	Thr	Gln	Thr	Leu	Asp	Ile	Val	Ala
						85			90			95			

Glu	Asn	Pro	Asp	Lys	Phe	Arg	Val	Val	Ala	Leu	Ala	Ala	Gly	Ser	Asn
						100		105				110			

Val Thr Leu Leu Ala Asp Gln Val Lys Thr Phe Lys Pro Lys Leu Val
 115 120 125
 Ala Val Arg Asn Glu Ser Leu Leu Asn Glu Leu Lys Glu Ala Leu Ala
 130 135 140
 Gly Cys Glu Glu Met Pro Glu Ile Ile Pro Gly Glu Gln Gly Val Ile
 145 150 155 160
 Glu Val Ala Arg His Pro Asp Ala Val Thr Val Val Thr Gly Ile Val
 165 170 175
 Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu Ala Gly Lys
 180 185 190
 Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly Gly Pro Phe
 195 200 205
 Val Leu Pro Leu Ala His Lys His Asn Val Lys Ile Leu Pro Ala Asp
 210 215 220
 Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu Ser Glu Gly
 225 230 235 240
 Ser Leu Arg Arg Val Ile Leu Thr Ala Ser Gly Gly Ala Phe Arg Asp
 245 250 255
 Trp Pro Val Glu Lys Leu Lys Asp Val Lys Val Ala Asp Ala Leu Lys
 260 265 270
 His Pro Asn Trp Ser Met Gly Lys Ile Thr Val Asp Ser Ala Thr
 275 280 285
 Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr Leu Phe Gly
 290 295 300
 Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His Pro Gln Ser Ile Ile
 305 310 315 320
 His Ser Met Ile Glu Thr Gln Asp Ser Ser Val Leu Ala Gln Leu Gly
 325 330 335
 Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr Leu Ser Trp Pro Asp
 340 345 350
 Arg Val Tyr Cys Ser Glu Val Thr Trp Pro Arg Leu Asp Leu Cys Lys
 355 360 365
 Leu Gly Ser Leu Thr Phe Lys Ala Pro Asp Asn Val Lys Tyr Pro Ser
 370 375 380
 Val Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly Gly Thr Met Thr Gly
 385 390 395 400
 Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu Leu Phe Ile Asp Glu
 405 410 415
 Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val Glu Met Thr Cys Asp
 420 425 430

Ala His Arg Asn Glu Leu Val Thr Arg Pro Ser Leu Glu Glu Ile Ile
 435 440 445

His Tyr Asp Gln Trp Ala Arg Lys Phe Ala Ala Asn Leu Gln Pro Ser
 450 455 460

Ser Ser Gly Arg Ser Pro Val Leu Ala
 465 470

<210> 21
 <211> 406
 <212> PRT
 <213> *Arabidopsis thaliana*

<400> 21
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Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Asp Ile Val Ala Glu Asn
 20 25 30

Pro Asp Lys Phe Arg Val Val Ala Leu Ala Ala Gly Ser Asn Val Thr
 35 40 45

Leu Leu Ala Asp Gln Val Arg Arg Phe Lys Pro Ala Leu Val Ala Val
 50 55 60

Arg Asn Glu Ser Leu Ile Asn Glu Leu Lys Glu Ala Leu Ala Asp Leu
 65 70 75 80

Asp Tyr Lys Leu Glu Ile Ile Pro Gly Glu Gln Gly Val Ile Glu Val
 85 90 95

Ala Arg His Pro Glu Ala Val Thr Val Val Thr Gly Ile Val Gly Cys
 100 105 110

Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu Ala Gly Lys Asp Ile
 115 120 125

Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly Gly Pro Phe Val Leu
 130 135 140

Pro Leu Ala Asn Lys His Asn Val Lys Ile Leu Pro Ala Asp Ser Glu
 145 150 155 160

His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu Pro Glu Gly Ala Leu
 165 170 175

Arg Lys Ile Ile Leu Thr Ala Ser Gly Gly Ala Phe Arg Asp Trp Pro
 180 185 190

Val Glu Lys Leu Lys Glu Val Lys Val Ala Asp Ala Leu Lys His Pro
 195 200 205

Asn Trp Asn Met Gly Lys Lys Ile Thr Val Asp Ser Ala Thr Leu Phe
 210 215 220

Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr Leu Phe Gly Ala Glu
 225 230 235 240

Tyr Asp Asp Ile Glu Ile Val Ile His Pro Gln Ser Ile Ile His Ser
 245 250 255
 Met Ile Glu Thr Gln Asp Ser Ser Val Leu Ala Gln Leu Gly Trp Pro
 260 265 270
 Asp Met Arg Leu Pro Ile Leu Tyr Thr Met Ser Trp Pro Asp Arg Val
 275 280 285
 Pro Cys Ser Glu Val Thr Trp Pro Arg Leu Asp Leu Cys Lys Leu Gly
 290 295 300
 Ser Leu Thr Phe Lys Lys Pro Asp Asn Val Lys Tyr Pro Ser Met Asp
 305 310 315 320
 Leu Ala Tyr Ala Ala Gly Arg Ala Gly Gly Thr Met Thr Gly Val Leu
 325 330 335
 Ser Ala Ala Asn Glu Lys Ala Val Glu Met Phe Ile Asp Glu Lys Ile
 340 345 350
 Ser Tyr Leu Asp Ile Phe Lys Val Val Glu Leu Thr Cys Asp Lys His
 355 360 365
 Arg Asn Glu Leu Val Thr Ser Pro Ser Leu Glu Ile Val His Tyr
 370 375 380
 Asp Leu Trp Ala Arg Glu Tyr Ala Ala Asn Val Gln Leu Ser Ser Gly
 385 390 395 400
 Ala Arg Pro Val His Ala
 405
 <210> 22
 <211> 475
 <212> PRT
 <213> *Mentha x piperita*
 <400> 22
 Met Ala Leu Asn Leu Met Ala Pro Thr Glu Ile Lys Thr Leu Ser Phe
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 Leu Asp Ser Ser Lys Ser Asn Tyr Asn Leu Asn Pro Leu Lys Phe Gln
 20 25 30
 Gly Gly Phe Ala Phe Lys Arg Lys Asp Ser Arg Cys Thr Ala Ala Lys
 35 40 45
 Arg Val His Cys Ser Ala Gln Ser Gln Ser Pro Pro Pro Ala Trp Pro
 50 55 60
 Gly Arg Ala Phe Pro Glu Pro Gly Arg Met Thr Trp Glu Gly Pro Lys
 65 70 75 80
 Pro Ile Ser Val Ile Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu
 85 90 95
 Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Ile Val Ala Leu Ala
 100 105 110

Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Lys Ala Phe Lys Pro
 115 120 125

Lys Leu Val Ser Val Lys Asp Glu Ser Leu Ile Ser Glu Leu Lys Glu
 130 135 140

Ala Leu Ala Gly Phe Glu Asp Met Pro Glu Ile Ile Pro Gly Glu Gln
 145 150 155 160

Gly Met Ile Glu Val Ala Arg His Pro Asp Ala Val Thr Val Val Thr
 165 170 175

Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu
 180 185 190

Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly
 195 200 205

Gly Pro Phe Val Leu Pro Leu Ala Lys Lys His Asn Val Lys Ile Leu
 210 215 220

Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu
 225 230 235 240

Pro Glu Gly Ala Leu Arg Arg Ile Ile Leu Thr Ala Ser Gly Gly Ala
 245 250 255

Phe Arg Asp Leu Pro Val Glu Lys Leu Lys Glu Val Lys Val Ala Asp
 260 265 270

Ala Leu Lys His Ser Asn Trp Asn Met Gly Lys Lys Asn Thr Val Arg
 275 280 285

Leu Leu Gln Leu Phe Phe Asn Lys Gly Leu Glu Val Ile Lys Ala His
 290 295 300

Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His Ser
 305 310 315 320

Pro Ser Ile Ile His Ser Met Val Glu Thr Gln Asp Ser Ser Val Leu
 325 330 335

Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr Leu
 340 345 350

Ser Trp Pro Glu Arg Val Tyr Cys Ser Glu Ile Thr Trp Pro Arg Leu
 355 360 365

Asp Leu Cys Lys Val Asp Leu Pro Phe Lys Lys Pro Asp Asn Arg Glu
 370 375 380

Ile Pro Ala Met Asp Leu Ala Tyr Ala Ala Trp Lys Ser Arg Ser Thr
 385 390 395 400

Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu Met Phe
 405 410 415

Ile Asp Glu Lys Ile Gly Tyr Leu Asp Ile Phe Lys Val Val Glu Leu
 420 425 430

Thr Cys Asp Lys His Arg Ser Glu Met Ala Val Ser Pro Ser Leu Glu
435 440 445

Glu Ile Val His Tyr Asp Gln Trp Ala Arg Asp Tyr Ala Ala Thr Val
450 455 460

Leu Lys Ser Ala Gly Leu Ser Pro Ala Leu Val
465 470 475